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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 01:32:29 ; Search time 793.194 Seconds
(without alignments)
822.965 Million cell updates/sec

Title: US-09-856-979-6
Perfect score: 1695
Sequence: 1 ccgcagatcctctgtgtga.....tccatcaagccgtcgcgatg 1695

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695	100.0	5349	10	US-09-970-921-7 Sequence 7, Appli
2	1695	100.0	6539	9	US-09-509-945-5 Sequence 5, Appli
3	1695	100.0	6548	9	US-09-509-945-4 Sequence 4, Appli
4	72.6	4.3	965	10	US-09-770-445-298 Sequence 298, App
5	70.6	4.2	828	9	US-09-938-842A-1513 Sequence 1513, Ap
6	67	4.0	816	9	US-09-938-842A-2155 Sequence 2155, Ap
7	60	3.5	293	10	US-09-294-093B-2837 Sequence 2837, Ap
8	59.6	3.5	709	10	US-09-770-149-213 Sequence 213, App
9	56	3.3	440	10	US-09-878-574-4918 Sequence 4918, Ap
10	53.6	3.2	304	10	US-09-294-093B-3541 Sequence 3541, Ap
11	47.8	2.8	367	10	US-09-770-791-415 Sequence 415, App
12	36.6	2.2	396	10	US-09-878-574-1420 Sequence 1420, Ap
13	36.2	2.1	2573	10	US-09-917-800A-1339 Sequence 1339, Ap
14	36	2.1	6021	10	US-09-819-247-1 Sequence 1, Appli
15	35.8	2.1	65359	10	US-09-804-472-3 Sequence 3, Appli
16	35.6	2.1	382	10	US-09-878-574-5334 Sequence 5334, Ap
17	35.6	2.1	29793	10	US-09-973-451-38 Sequence 38, Appl
18	35	2.1	1241	12	US-10-044-090-274 Sequence 274, App
19	34.8	2.1	458	10	US-09-764-877-687 Sequence 687, App

20	34.8	2.1	475	10	US-09-560-863-101	Sequence 101, App
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c 22	34.6	2.0	3824	10	US-09-764-869-2167	Sequence 2167, Ap
c 23	34.4	2.0	1139	9	US-09-938-842A-3856	Sequence 3856, Ap
24	34.2	2.0	3400	10	US-09-987-025-1	Sequence 1, Appli
25	34.2	2.0	640681	10	US-09-790-988-1	Sequence 1, Appli
c 26	34	2.0	821	10	US-09-878-574-4653	Sequence 4653, Ap
c 27	33.6	2.0	390	10	US-09-880-107-459	Sequence 459, App
28	33.6	2.0	432	10	US-09-960-352-3329	Sequence 3329, Ap
c 29	33.6	2.0	775	10	US-09-834-975-749	Sequence 749, App
30	33.2	2.0	375	10	US-09-864-761-11762	Sequence 11762, A
31	32.8	1.9	643	12	US-10-044-090-812	Sequence 812, App
c 32	32.8	1.9	147309	10	US-09-742-312-3	Sequence 3, Appli
c 33	32.8	1.9	170834	10	US-09-835-232-7	Sequence 7, Appli
34	32.6	1.9	2000	9	US-09-938-842A-4909	Sequence 4909, Ap
c 35	32.6	1.9	5970	9	US-10-108-605-210	Sequence 210, App
c 36	32.6	1.9	6282	9	US-10-108-605-212	Sequence 212, App
37	32.6	1.9	12932	10	US-09-764-847-1132	Sequence 1132, Ap
38	32.6	1.9	53332	10	US-09-801-861-3	Sequence 3, Appli
c 39	32.4	1.9	253	10	US-09-878-574-14973	Sequence 14973, A
c 40	32.4	1.9	2000	9	US-09-938-842A-3048	Sequence 3048, Ap
c 41	32.4	1.9	3793	10	US-09-881-752A-149	Sequence 149, App
c 42	32.4	1.9	32190	10	US-09-764-877-2844	Sequence 2844, Ap
c 43	32.2	1.9	337	9	US-10-040-739-195	Sequence 195, App
c 44	32.2	1.9	374	10	US-09-983-965-4954	Sequence 4954, Ap
45	32.2	1.9	1895	10	US-09-764-864-230	Sequence 230, App

ALIGNMENTS

RESULT 1
US-09-970-921-7
; Sequence 7, Application US/09970921
; Patent No. US2002013845A1
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "T-DNA of pTTS243"
; NAME/KEY: misc_feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: label = RB, "T-DNA right border"
; NAME/KEY: misc_feature
; LOCATION: Complement((98)..(331))
; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
; NAME/KEY: misc_feature
; LOCATION: Complement((332)..(883))
; OTHER INFORMATION: label = bar, "region coding for phosphinethricin
; OTHER INFORMATION: acetyl transferase"
; NAME/KEY: misc_feature
; LOCATION: Complement((884)..(2258))
; OTHER INFORMATION: label = p35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: Virus"
; NAME/KEY: misc_feature
; LOCATION: (2281)..(3969)
; OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO
; OTHER INFORMATION: 92/13956)"
; NAME/KEY: misc_feature
; LOCATION: (3970)..(4245)
; OTHER INFORMATION: label = synb*, "improved barstar DNA"
; NAME/KEY: misc_feature

; LOCATION: (4246)..(4577)									
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated									
; OTHER INFORMATION: end of chalcone synthase gene"									
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; LOCATION: Complement((5325)..(5349))									
; OTHER INFORMATION: label = LB, "T-DNA left border"									
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0;									
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Qy	61	AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCCAATCGCCGACAATACCAATAGAGA	120						
Db	2338	AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCCAATCGCCGACAATACCAATAGAGA	2397						
Qy	121	TCCAACCACCTTAATATCATATAACAATCTGATTGTTAGTCCAGAACTATATTGAGTAGTG	180						
Db	2398	TCCAACCACCTTAATATCATATAACAATCTGATTGTTAGTCCAGAACTATATTGAGTAGTG	2457						
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Db	2518	GATGCTCTAATCTGGTCAATTTTAGCGCTCCAGAAAGAATGCAACAATCCTTGGACAAT	2577						
Qy	301	GTTGGCACTGGAACCTGTTGCATGTTTTTACATCTCTTATTAACGTAGCAAAAGGAGTAGAT	360						
Db	2578	GTTGGCACTGGAACCTGTTGCATGTTTTTACATCTCTTATTAACGTAGCAAAAGGAGTAGAT	2637						
Qy	361	TATTATGTACCAGGAGAAATCTCTTCAGATCCCTTCCACATGCAATGTCGTAAGAACAG	420						
Db	2638	TATTATGTACCAGGAGAAATCTCTTCAGATCCCTTCCACATGCAATGTCGTAAGAACAG	2697						
Qy	421	ATACAGTGTACGTTAGTTTGTAAATGGACGGTCAATGGCCATTTCTCTGAAGGCATGTTT	480						
Db	2698	ATACAGTGTACGTTAGTTTGTAAATGGACGGTCAATGGCCATTTCTCTGAAGGCATGTTT	2757						
Qy	481	AGATGATGATTTCTGGGATCCCTTGGAGGGCCCTGAAATTCGGAACAGTTAGTTGAGTT	540						
Db	2758	AGATGATGATTTCTGGGATCCCTTGGAGGGCCCTGAAATTCGGAACAGTTAGTTGAGTT	2817						
Qy	541	TTAGTACCTAATGTCTTGCGTTATACACTACGTGAAATGCCATTTCTGTAAAGCTGAGTTTC	600						
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Qy	721	TCTACTACATCGAACAGGAACCATATCAATGTTGCCCCCAGCAAGGACCCCGCAGATAAG	780						
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Qy	841	ACCACATCGGCTCAGAGAGAAGTTATGATAAAGGCCTAATCTCTGAATAATTCTCTAGA	900						
Db	3118	ACCACATCGGCTCAGAGAGAAGTTATGATAAAGGCCTAATCTCTGAATAATTCTCTAGA	3177						
Qy	901	AAGCGAATAATAATAGCACACCTTGACCTCCACCAAGAAGCTTGTGGATCGACTTGTGCC	960						

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Qy	961	CATGAAATGGCATTTCTGACATTTCTGGTCACCTGTGCAGAAATCTCTCGGAAATGAGGAGCA	1020
Db	3238	CATGAAATGGCATTTCTGACATTTCTGGTCACCTGTGCAGAAATCTCTCGGAAATGAGGAGCA	3297
Qy	1021	TAGCTTCGTGTGTATGTGTGGGATATTACGGCTGCTAAACCTTTGTGTTTCTGTATCG	1080
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Qy	1561	GCTTGCACCGTGACTCACTGCCACATTTGCCCGCCCGCTCGCCGGCGGCTACAAAAGCCA	1620
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Qy	1621	CACACGCACGCCGCCACGATAACCCATCCTPAGCATCCCGGTGTCCAGCAAGAGATCCAT	1680
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RESULT 2
US-09-509-945-5/c
; Sequence 5, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID G
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6539
; TYPE: DNA
; ORGANISM: Escherichia.coli LE392
; FEATURE:

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Clone: pts431
US-09-509-945-5

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAAATCGCGACAAATACCAATAGAGA 120
Db 4247 AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAAATCGCGACAAATACCAATAGAGA 4188

Qy 121 TCCAAACACCTTAATATATATAAACAATCTGATTTGTTAGTCCAGAACTATATENGTAGTG 180
Db 4187 TCCAAACACCTTAATATATATAAACAATCTGATTTGTTAGTCCAGAACTATATENGTAGTG 4128

Qy 181 AACAAATAGCAATTAACATTAATGAGGATTAATGGCTAACTCTGCAATTAATTAATTTCT 240
Db 4127 AACAAATAGCAATTAACATTAATGAGGATTAATGGCTAACTCTGCAATTAATTAATTTCT 4068

Qy 241 GATGCTCTAATCTGGTCAATTTTAGCGCTCCAGAAAGAAATTCGACAAATCCTTGGACAAT 300
Db 4067 GATGCTCTAATCTGGTCAATTTTAGCGCTCCAGAAAGAAATTCGACAAATCCTTGGACAAT 4008

Qy 301 GTTGGCACTGGAATGTTGCAATGTTTACATCTCTTATTAACSTAGCAAGAGTAGAT 360
Db 4007 GTTGGCACTGGAATGTTGCAATGTTTACATCTCTTATTAACSTAGCAAGAGTAGAT 3948

Qy 361 TATTATGTACCAAGAGAAATCTCTTCAGATCCTTTCCACATGCAATTCGTAAGAACAG 420
Db 3947 TATTATGTACCAAGAGAAATCTCTTCAGATCCTTTCCACATGCAATTCGTAAGAACAG 3888

Qy 421 ATACAGTGTACGTTAGTTGTAATGGACGGTCAATGCCATTTCTCTGAAGGCAATGTTTCAG 480
Db 3887 ATACAGTGTACGTTAGTTGTAATGGACGGTCAATGCCATTTCTCTGAAGGCAATGTTTCAG 3828

Qy 481 AGATGATGATTTCTGGGATCCTTGGAGGGGCCCTGAAATTCGGAACAGTTAGTTAGTT 540
Db 3827 AGATGATGATTTCTGGGATCCTTGGAGGGGCCCTGAAATTCGGAACAGTTAGTTAGTT 3768

Qy 541 TTAGTACCTAATGCTTGGGTTATACCTGTAAGTAAATGCCATTTCTGTAAGCTGATTTTC 600
Db 3767 TTAGTACCTAATGCTTGGGTTATACCTGTAAGTAAATGCCATTTCTGTAAGCTGATTTTC 3708

Qy 601 TACCATCTCCACAGGAAATAAAGCTAATACCTGTCGAAGAGTGGCGGCAATTCGACCAA 660
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Qy 661 ATGAAGATCACAGCATGGCAAGAAATGGCAATCTGGCAAGAGGCGGAATTAATTTGAT 720
Db 3647 ATGAAGATCACAGCATGGCAAGAAATGGCAATCTGGCAAGAGGCGGAATTAATTTGAT 3588

Qy 721 TCTACTACATCGAACAGGAACCATATCAATGTTGCCCGCAGCAAGGACCCCGCAGATAAG 780
Db 3587 TCTACTACATCGAACAGGAACCATATCAATGTTGCCCGCAGCAAGGACCCCGCAGATAAG 3528

Qy 781 TTCCTGTTCTTCCACAGCAGAAATATCCGCAACTGCATAGCTCCCAACAATGAATCCAAA 840
Db 3527 TTCCTGTTCTTCCACAGCAGAAATATCCGCAACTGCATAGCTCCCAACAATGAATCCAAA 3468

Qy 841 ACCACATCGGGCTCAGAGAGAGTATGATGATAAAGGCACTAATTCGAAATAATTCCTAGA 900
Db 3467 ACCACATCGGGCTCAGAGAGAGTATGATGATAAAGGCACTAATTCGAAATAATTCCTAGA 3408

Qy 901 AAGCGAATAATAATAGCACACCTTGGACCTCCACCAAGAACCTTGTGGATCGACTTGTGCC 960
Db 3407 AAGCGAATAATAATAGCACACCTTGGACCTCCACCAAGAACCTTGTGGATCGACTTGTGCC 3348

Qy 961 CATGAAATGGCAATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTG 1020
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Qy 1081 ATCTGTTTAGAGAGCATCGCTTTATATAGCACTTAAATAAGTGTAGTATATCTCTCAAG 1140
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Db 2927 CACGTAAGGTCCTACACTCAACCTAACHTGTGTAACGCTCTGTTCTGGCCACGGTGAG 2868
Qy 1441 AATGACACTAATGGACGGGCAACACACTTCTTTCAACGCTGCTACTGCTATCTGCTAGAC 1500
Db 2867 AATGACACTAATGGACGGGCAACACACTTCTTTCAACGCTGCTACTGCTATCTGCTAGAC 2808
Qy 1501 GGTGGACGCGTGAGTGCTTTCGCCCATGACCGCTCTGTTGTTGTCAGTCACTTGGCAC 1560
Db 2807 GGTGGACGCGTGAGTGCTTTCGCCCATGACCGCTCTGTTGTTGTCAGTCACTTGGCAC 2748
Qy 1561 GCTTGACCGTGACTCACTGCAACATGTCACCATGTCGCGCTGCGGCGCTTACAAAAGCCA 1620
Db 2747 GCTTGACCGTGACTCACTGCAACATGTCACCATGTCGCGCTGCGGCGCTTACAAAAGCCA 2688
Qy 1621 CACACGACGCGGCGCACGATACCCATCCCTAGCATCCCGGTGTCAGCAAGAGATCCAT 1680
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Qy 1681 CAAGCCGTCGCGATG 1695
Db 2627 CAAGCCGTCGCGATG 2613
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RESULT 3
US-09-509-945-4/c
; Sequence 4, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID G
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Escherichia coli LE392
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Clone: pts172
US-09-509-945-4
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; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 298
; LENGTH: 965
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(965)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-298

Query Match      4.3%; Score 72.6; DB 10; Length 965;
Best Local Similarity 60.3%; Pred. No. 2.1e-11;
Matches 120; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 612 CAGGAAATAAGCTAATACCTGTCCAAAGAGTGGTGGCGCATTTGACCAAAATGAAGATCAC 671
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Db 465 CGGGATGTGAGGAGTTGACTGTGGATGAATGTACAAGCATTAGACCACAAGAACAATGC 406

QY 672 AAGCATGGCAAGAAATGGCAATCTGGCCAAAGGAGCGGAATATATATTGTATTTCTACTACATC 731
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 405 TGCAAGAGCAAAATCGCAAGGTGACAGAGAAAAGCGGAGATGGTATTCGAATAACTC 346

QY 732 GAACAGGAACCATATCAATGTGCCCCAGCAAGGACCCCGCAGATAAGTTCCCTGTTCCT 791
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 345 GAATAAGACCCCAAGACGCGAGTTACAGCACCCCAAGACTCCACCAGATACCTTCTTGTTCCT 286

QY 792 CCACAGCAGAAATATCCGCA 810
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 CCAAGGAATATATCAGCA 267

RESULT 5
US-09-938-842A-1513/c
; Sequence 1513, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1513
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1513

Query Match      4.2%; Score 70.6; DB 9; Length 828;
Best Local Similarity 61.9%; Pred. No. 7.4e-11;
Matches 112; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 629 ACCTGTCCAAGAGTGGTGGCGCATTTTGACCAAAATGAAGATCACAAAGCATGGCAAGATGG 688
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 448 ACTTGTTAATGAACATAGTGGCATTAGACCACAAAAACAGACACAGCGAGAACAAACAATCA 389
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QY 689 CAATCTGGCAAAGGAGCGGAATTATATTGTATTCTACTACATCGAACAGGAACCATATCA 748
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 388 TCACGTGGCAAAGCAGAGTGAGAAAGATGGTACTCCATCAATTCAAACACAACCCCAAGCAG 329

QY 749 ATGTTGCCCCCAGCAGGACCCCGCAGAGATAAGTTCTGTCTCTTCCACAGCAGAAATATCCG 808
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 328 CTGTAGCACCACCACCAAGTACACCACCAGACATCTTCTTGTCTTCTCCACATGAATATATCAG 269

QY 809 C 809
|
Db 268 C 268

RESULT 6
US-09-938-842A-2155/c
; Sequence 2155, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2155
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2155

Query Match      4.0%; Score 67; DB 9; Length 816;
Best Local Similarity 55.3%; Pred. No. 8.6e-10;
Matches 130; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 627 ATACCTGTCCAAGAGTGGTGGCGCATTTTGACCAAAATGAAGATCAAGCATGGCAAGAAT 686
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 438 AGACTGTGTAATGAACATAGTGGCATTAGACCATAGAAAACAACACAGCAAGGCAACGAT 379

QY 687 GGCAATCTGGCAAAGGAGCGGAATTATATTGTATTCTACTACATCGAAACAGGAACCATAT 746
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 378 CATAAGCTGACATAACAGAGTAAGAAGATGATCTCCATCAATTCAAAATAGCACCCTATGC 319

QY 747 CAATGTTGCCCCAGCAGGACCCCGCAGAGATAAGTTCTGTCTTCCACAGCAGAAATATC 806
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 318 CACTGTAGCACCAGCAAAATACACCTCTGACATTTTCTTGTCTTCCACATATATATC 259

QY 807 CGCAACTGCATAGCTCCCAACAATGAATCCAAARCCACATCGGGTCAGAGAGAA 861
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 258 TGCCGGTTTTCCGCCCGCGAGAACCTTATGAACAGGGTCTCTCTCTTCCGAACAA 204

RESULT 7
US-09-294-093B-2837/c
; Sequence 2837, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
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; SEQ ID NO 3541
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700380432H1
;
; NAME/KEY: unsure
; LOCATION: 31, 46, 65, 154, 185
; OTHER INFORMATION: a, t, c, g, or other
;
US-09-294-093B-3541

Query Match          3.2%; Score 53.6; DB 10; Length 304;
Best Local Similarity 66.4%; Pred. No. 4.4e-06;
Matches 77; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 694 TGGCAAGGACGGGAATTATATTGTATTCTACTACATCGAACAGGACCATATCAATGTT 753
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 304 TGGCACACCAAGGTGAGGAGATGGTACTCCATAACCTCGAACAGGAGCCAGATGCCCGTG 245

Qy 754 GCCCAGCAAGGACCCCGCGACATAAGTTCCTGTTCTTCCACAGCAGAATATCCGC 809
      || ||||| || ||||| | || | || ||||| |||| | | | || || || ||
Db 244 GCACCAGCGAGTACCCCGCTGAGATCTTCTTGTTCCTCCATAGGACAAGATCGGC 189

RESULT 11
US-09-770-791-415/c
; Sequence 415, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 415
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-415

Query Match          2.8%; Score 47.8; DB 10; Length 367;
Best Local Similarity 57.8%; Pred. No. 0.00025;
Matches 85; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 664 AAGATCACAGCATGGCAAGAATGCGAATCTGGCAAAGGAGCGGAATTATATTGTATTCT 723
      |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 364 AAGAGGCCTCAAGAGCGAGTATCGAAATGTGACACAAAAGACTCAACAAATGATACTCA 305

Qy 724 ACTACATCGAACAGGAACCATATATCAATGTTGCCCCAGCAAGGACCCCGCGAGATAAGTTC 783
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Db 304 ACCAGCTCGAACAGAACCCAAATAGCAGTCGCGCACCAAGAACAGCACCTGATAGTTT 245
      || | ||||| | ||| | | || | | |||| | | |||| | |
Qy 784 CTGTTCTTCCACAGCAGAGAATATCCGCA 810
      | | | ||||| | | ||| |||
Db 244 TTATCCCTCCACAAGAACAACATCAGCA 218

RESULT 12
US-09-878-574-1420/c
; Sequence 1420, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1420
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-038-Q1-B1-B2
US-09-878-574-1420

Query Match          2.2%; Score 36.6; DB 10; Length 396;
Best Local Similarity 57.4%; Pred. No. 0.55;
Matches 66; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 721 TCTACTACATCGAACAGAACCATATCAATGTTGCCCGCAGCAAGGACCCCGCAGATAAG 780
      || | | ||||| |||| | ||| | | |||| | | |||| |
Db 395 TCAAGCAAGTCAAAAAGAACCCAAACAGCAGTGGCTCCGCCAAGCATGCCAGCAAAATT 336
      || | | ||||| |||| | ||| | | |||| | | |||| |
Qy 781 TTCCTGTTCTTCCACAGCAGAGAATATCCGCAACTGCATAGCTCCCAACAATGAAT 835
      || | |||| | |||| | | ||| || | | || | | | |
Db 335 TTCTGTTCTCTCCACAATAACACATCAGCAGGTTTTTCCGGCGCGAAACGGAGT 281
      || | |||| | |||| | | ||| || | | || | | | |

RESULT 13
US-09-917-800A-1339/c
; Sequence 1339, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
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; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1339
; LENGTH: 2573
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D42148
US-09-917-800A-1339

Query Match      2.1%; Score 36.2; DB 10; Length 2573;
Best Local Similarity 49.2%; Pred. No. 2.2;
Matches 95; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 318 TGCATGTTTTACATCTCTTATTAAAGGTAGCAAGGAGTAGATTATTATGTACCAGGAGA 377
Db 2508 TGCTTTTTTTCCTTCTCATACTCCAGTCCAATTGAGTGCAGCGGATATGCGTATGTAAA 2449

QY 378 AATCCTTCAGATCCCTTCCACATGCCAATGTCGTAAGAACAGATACAGTGTACGTTAGT 437
Db 2448 CATATCTTTAAAGCCGATCACCTTTAAGGTCAATTTAGAGAAAAAAAAGTCGTCTTGT 2389

QY 438 TTGTAATGGACGGTCAATGCCATTTCTCTGAAGGCATCTTCAGAGATGATGATTTCTGGG 497
Db 2388 TTCTGGTTTGTGTTGCCTGTCTGCGCGGAGGGTGTCTGCAGAGCAGTGTCAITCTGGA 2329

QY 498 ATCCTTGGAGGGG 510
Db 2328 AGGCTCTTTGGAG 2316

RESULT 14
US-09-819-247-1/c
; Sequence 1, Application US/09819247
; Patent No. US20010036635A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer Cel
; TITLE OF INVENTION: Alimentary Canal Origin
; FILE REFERENCE: TJU2413
; CURRENT APPLICATION NUMBER: US/09/819,247
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/192,229
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6021
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-819-247-1

Query Match      2.1%; Score 36; DB 10; Length 6021;
Best Local Similarity 45.9%; Pred. No. 4.2;
Matches 123; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 20 ATTGTTTTTATAAAATTTAATATTTATCTGGAFACCTACCAATATATAGTAGACTTGTG 79
Db 5888 ATAATTACATAAAAAATTTTATTTAAATTTAAAAATCACGTTTAAATTTATATCTTAGCTATT 5829

QY 80 AAGCTGCAAGAACTTCCAAATCGCCGACAATACCAATAGAGATCCAACCCCTTAATATCA 139
Db 5828 TACATACATGTTTAGTAACTAGTTTACAATTTGAGCTGATACTTAAACAAGGATAAATAGG 5769

QY 140 TAAACAATCTGATTTGTAGTCCAGAACTATATTGAGTAGTGAACAACAATAGCACATTAA 199
Db 5768 GCTATTCAAATTTTGTAAATATGCCTTAAATTTGAATCCAAGTCACATTACTATAATAA 5709

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QY 200 CATTATGAGGATTATTGGCTAACTCTGCAATTCAATATTCTGATGCGTCTAATCTGGTCA 259
Db 5708 AATTAGCATTATCATTTGATGTAGCTACAGCTACAAAATAACTTTTCGATGTTATGAAAGCTATAT 5649

QY 260 ATTTAGCGCTCCAGAAAAGAATTGCACA 287
Db 5648 TTTGTAGAGTACAAGAACCACCAAGTGAAGA 5621

RESULT 15
US-09-804-472-3/c
; Sequence 3, Application US/09804472
; Patent No. US20020143146A1
; GENERAL INFORMATION:
; APPLICANT: SHAO, Wei et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001163
; CURRENT APPLICATION NUMBER: US/09/804,472
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 65359
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(65359)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-472-3

Query Match      2.1%; Score 35.8; DB 10; Length 65359;
Best Local Similarity 47.9%; Pred. No. 20;
Matches 103; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 16 TGTGATTGTTTTTATAAAATTTAATATTTTATCTGGAATACCTTACCAATATATAGTAGACT 75
Db 62163 TGATTTTGTATTTCCAAAAAGTACTTTTATTGCTAAAAGATATTAAAAATTATCCAGCAACCA 62104

QY 76 TGTCAGCTGCAGAACTTCCAATCGCCGACAATACCAATAGAGATCCCAACCACCTTAAT 135
Db 62103 TCCTTTGGTATATAAAAGTTACTATGGTCACTAATAGTATGACAGCCTTTCCACCCGAGGT 62044

QY 136 ATCATAAACAACTCTGATTGTTAGTCCAGAACTATATTGAGTAGTGAAACAACAATAGCACA 195
Db 62043 CTGAGGACTGCATGCCCTCAATGAAGCAGAGCTATTTTGATTAAATGTATGCCCAACAAAAA 61984

QY 196 TTAACATTATGAGGATTATTGGCTAACTCTGCAAT 230
Db 61983 GTAACAAAAACTGGATGGATGTATGACTAGGAAAT 61949

Search completed: December 2, 2002, 04:18:26
Job time : 830.194 secs

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